

㈱日本触媒 基礎技術研究所 仙波 尚

Cassava 由来 SHNL の ^{Amino acid seq.} アミノ酸配列 (Gene Bank No. AJ223281)

MAVVDFVLIHTICHCAWIWYKLKPVLEAAGHKVLTALDLAASGVDPQRQIEQINSFDEYSEPLLTFMESLPQ
QEKVILVGESCGGLNIAAADKYPEKIAAAVFQNSLLPDTKIIKPSYVVDKLMFVFPDWKDTEYFEFSNSN
GETITGMVLGLKLMRENLYTICPPEDYELAKMLTRRGSLFQSILAQREKFTEKGYGSIKKIYVWTGDDKI
FLPEFQLWQJENYKPDVFRVMGGDIKQLTKTNEIAGILQKVADIYA

Prunus 由来 RHNL の ^{Amino acid seq.} アミノ酸配列 (Gene Bank No. AF043186)

MEKSTMSAVVLVLNLLVLHLQYSEVHSLANTSSEHDFGYLKFFVYNAVDLELECSYDYIIVGGGTSGCPLA
ATLSANYSVLVLERGTIATEYPNTLTVDGFAYNLQQQDDGKTPVERFVSJEDGIDNVRSLGGTTIINAGV
YARANESFYNNSGVWDLDLVNEAYEWVEDAIVYKPSNQSWQSITGTAFLVAGVHPDNGFGLVHEEGT
RLTGSTFDNSCTRHASDELNLKGDNDLKVAVEAAVQKIIESTESSGLTAVGVVYTDNSNGTSHRALVSGK
GEVILSAGTLGTPQLLLLSGVGPESYLTSLNISVVASHPYVQYVNDNPRNFILPPNPIEPSTVTVLGITS
DFYQCSLSSLFPDTPPFSLFPTTSYPLPNQTFATVSKVPGPLSAGSLTLQSSSNVSVAPNVKFNYSDFV
DLTHCVSGMKKIGVFLSTDALKPYKVDDLPIDGFMILGTPLPENQTDAAFEKFCRDTVASVWHYHGG
AIVGKVIDGNFRVTGINALRVVDGSTFPATPASHPPQGFYLMGGRYVGTIVQERSASGEAHTSTFKPKLM
DSLKSALSFAF

両者のホモロジー検索結果

[GENETYX : Maximum Matching]

Date : 2002.12.17

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Sequence 1 : M.esculenta SHNL AA seq
Size : 258
Matching Position : 1 - 258

Sequence 2 : P.serotina RHNL AA seq
Size : 574

Matching Position : 1 - 574

Matching Condition.

Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 15.68 [%]
Weight : 456

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1 : M-----AVV -DFVL--IHT ICH----- --GAWIWKYKL KPV----- LE-----
    *      ***      *      *      *      *      *      *
1 : MEKSTMSAVV LVLNLLVLHL QYSEVHSLAN TSSEHDFGYL KFYVNAVDLE LEGSYDYIIV

28 : ----- --AA----- --GHKVT- ----- ALDLAASGVD PRQIEQINSF
    *      *      *      *      *      *
61 : GGGTSGCPLA ATLSANYSVL VLERGTIATE YPNTLTVDGF AYNLQQQDDG KTPVERFVSE

55 : D----EYSEP L----- --LTFMESLP QGEKV----I LVGESCGGLN IAI-----
    *      *      *      **      *      *      *
121 : DGIDNVRMRI LGGTTIINAG VYARANESFY NNSGVEWDLD LVNEAYEWVE DAIVYKPSNQ

89 : ----- -AADKYPEKI AAIV----- -----FQNS- -----LL- ---PD-----
    *      *      *      *      *      *
181 : SWQSITGTAF LEAGVHPDNG FGLVHBEGTR LTGSTFDNSG TRHASDELLN KGDPDNLKVA

110 : -----TKHKP SYVVDKLMEV FPDWKD----- -----TEYF EFSNSNGETI TGMVLGL---
    *      *      *      *      *      *      *
241 : VEAIVQKIIF STESSGLTAV GVYITDSNGT SHRALVSGKG EVILSAGTIG TPQLLLLSGV
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152 : -----KLMREN LYTICPPEDY E-----
      * * * * *

301 : GPESYLTSLN ISVVASHPYV GOYVNDNPRN FINILPPNPI EPSTVTVLGI TSDFYQCSLS

169 : LAKMLTRRGS LF----- --QS---IL AQREKF---
      * * * * *

361 : SLFFDTPPFS LFPTTSYPLF NQTFHIVSK VPGPLSAGSL TLQSSSNVSV APNVKFNYS

191 : -----TEKGY GSIK----- ----KIYV-- -WIGDD---- -KIFLPEFQ- -----
      * * * * *

421 : DPVDLTHCVS GMKKIGVFLS TDALKPYKVD DLPGIDGFNI LGTPLPENQT DDAAFEKFCR

217 : -----LWQIENYKPD LVFRVMG--- -----GDH KLQL-----T
      * * * * *

481 : DTVASYWHYH GGAIVGKVID GNFRVTIGINA LRVVDGSTFP ATPASHPQGF YLMLGRYVGT

242 : K-----TNEIAG IL---QKVAD IYA-
      * * * * *

541 : KIVQERSASG EAIHTSTFKP KLMDSLKSAL SFAF

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[GENETYX : Amino Acid Sequence Homology Data]

Date : 2002.12.17

1st Amino Acid Sequence

File Name : Cassava SHNL AA seq.

Sequence Size : 258

2nd Amino Acid Sequence

File Name : P.serotina RHNL AA seq

Sequence Size : 574

Unit Size to Compare = 2

Pick up Location = 1

[31.818% / 22 aa] INT/OPT.Score : < 21/ 63 >

1' MAVVDFVLIIH TICHGAWIWY KKKPVLEAAG HKVTALDLAA SGVDPRQIEQ INSFDEYSEP

1"

MEKS TMSAVVLVLN LLVLHLQYSE

61' LLTFMESLPQ GEKVILVGES CGGLNIAIAA DKYPEKIAAA VFQNSLLPDT KHKPSYVVDK

25" VHSLANTSSE HDFGYLKFEVY NAVDLELEGS YDYIIVGGCT SGCPLAATLS ANYSVLVLER

121' LMEVFPDWKD TEYFEFSNSN GETITGMVLG LKLMRENLYT ICPPEDYELA KMLTRRGSLE

85" GTIATEYPNT LTVDFGAYNL QQQDDGKTPV ERFVSEDGID NVRSRILGGT TIINAGVYAR

181' QSILAQREKF TEKGYGSIKK IYVWTGDDKI FLPEFQLWQI ENYKPDVFR VMGGDHKLQL

... * * . . . * . * * *

145" ANESFYNNNSG VEWDLDLVNE AYEVEDAIV YKPSNQSWQS ITGTAFLEAG VHPDNGFGLV

241' TKTNEIAGIL QKVADIYA

205" HEEGTRLTGS TFDNSGTRHA SDELLNKGDP DNLKVAVEAA VQKIIFSTES SGLTAVGVVY